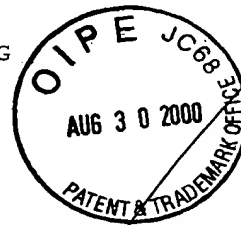


SEQUENCE LISTING



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(1) GENERAL INFORMATION:

(i) APPLICANT: RICCARDI, Carlo

(ii) TITLE OF INVENTION: INTRACELLULAR MODULATORS OF APOPTIC CELL DEATH PATHWAYS

(iii) NUMBER OF SEQUENCES: 15

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
- (B) STREET: 624 Ninth Street, N.W., Suite 300
- (C) CITY: Washington
- (D) STATE: D.C.
- (E) COUNTRY: USA
- (F) ZIP: 20001

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: 09/403,861
- (B) FILING DATE: 11-FEB-2000

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: PCT/EP98/02490
- (B) FILING DATE: 27-APR-1998

vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: EP 97107033.9
- (B) FILING DATE: 28-APR-1997

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: YUN, Allen C.
- (B) REGISTRATION NUMBER: 37,971
- (C) REFERENCE/DOCKET NUMBER: RICCARDI=1

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 202-628-5197
- (B) TELEFAX: 202-737-3528

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1972 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 206..616

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CTGGCTGCTG TGGAGTTTGT GACATACTAG GTGACACCCT TGGAGTCACT TCTCTTCAAC 60  
TCCAGCTTAG AAGTGCCTGC CTGGCTCAGG GTCTGCACTG CAGCCTACTC CTTGCTTCAG 120  
GGCCTGACTG CAACGCCAAA GCCTATCCTA TAGCGGCAGC GCCAGCAGCC ACTCAAACCA 180  
GCCACAGCTC CCCGGCAACC GAACC ATG AAC ACC GAA ATG TAT CAG ACC CCC 232  
Met Asn Thr Glu Met Tyr Gln Thr Pro  
1 5  
ATG GAG GTG GCG GTC TAT CAG CTG CAC AAT TTC TCC ACC TCC TTC TTT 280  
Met Glu Val Ala Val Tyr Gln Leu His Asn Phe Ser Thr Ser Phe Phe  
10 15 20 25  
TCT TCT CTG CTT GGA GGG GAT GTG GTT TCC GTT AAA CTG GAT AAC AGT 328  
Ser Ser Leu Leu Gly Gly Asp Val Val Ser Val Lys Leu Asp Asn Ser  
30 35 40  
GCC TCC GGA GCC AGT GTG GTG GCC CTA GAC AAC AAG ATT GAG CAG GCC 376  
Ala Ser Gly Ala Ser Val Val Ala Leu Asp Asn Lys Ile Glu Gln Ala  
45 50 55  
ATG GAC CTC GTG AAG AAC CAC CTG ATG TAC GCT GTG AGA GAG GAG GTG 424  
Met Asp Leu Val Lys Asn His Leu Met Tyr Ala Val Arg Glu Glu Val  
60 65 70  
GAG GTC CTA AAG GAG CAG ATT CGT GAG CTG CTT GAG AAG AAC TCC CAG 472  
Glu Val Leu Lys Glu Gln Ile Arg Glu Leu Leu Glu Lys Asn Ser Gln  
75 80 85  
CTG GAG CGC GAG AAC ACC CTC CTG AAG ACG CTG GCA AGC CCC GAG CAA 520  
Leu Glu Arg Glu Asn Thr Leu Leu Lys Thr Leu Ala Ser Pro Glu Gln  
90 95 100 105  
CTG GAA AAG TTC CAG TCC CGG CTG AGC CCT GAA GAG CCA GCA CCT GAA 568  
Leu Glu Lys Phe Gln Ser Arg Leu Ser Pro Glu Glu Pro Ala Pro Glu  
110 115 120  
GCC CCA GAA ACC CCG GAA ACC CCG GAA GCC CCT GGT GGT TCT GCG GTG 616  
Ala Pro Glu Thr Pro Glu Thr Pro Glu Ala Pro Gly Gly Ser Ala Val  
125 130 135  
TAAGTGGCTC TGTCCTTAGG GTGGGCAGAG CCACATCTTG TTCTACCTAG TTCTTTCCAG 676  
TTTGTTTTTG GCTCCCCAAG GGTCACTCTCA TGTGGAGAAC TTTACACCTA ACATAGCTGG 736  
TGCCAAGAGA TGTCCCAAGG ACATGCCCCT CTGGGTCCAC TCCAGTGACA GACCCCTGAC 796  
AAAGAGCAGG TCTCTGGAGA CTAAGTTGCA TGGGGCCTAG TAACACCAAG CCAGTGAGCC 856  
TGTCGTGTCA CCGGGCCCTG GGGGCTCCCA GGGCTGGGCA ACTTAGTTAC AGCTGACCAA 916  
GGAGAAAGTA GTTTTGAGAT GTGATGCCAG TGTGCTCCAG AAAGTGTAAG GGGTCTGTTT 976  
TTCATTTCCA TGGACATCTT CCACAGCTTC ACCTGACAAT GACTGTTCCT ATGAAGAAGC 1036  
CACTTGTGTT CTAAGCAGAA GCAACCTCTC TCTTCTTCCT CTGTCTTTTC CAGGCAGGGG 1096  
CAGAGATGGG AGAGATTGAG CCAAATGAGC CTTCTGTTGG TTAATACTGT ATAATGCATG 1156  
GCTTTGTGCA CAGCCAGTG TGGGGTTACA GCTTTGGGAT GACTGCTTAT AAAGTTCTGT 1216

TTGGTTAGTA TTGGCATCGT TTTTCTATAT AGCCATAATG CGTATATATA CCCATAGGGC 1276  
TAGATCTATA TCTTAGGGTA GTGATGTATA CATATACACA TACACCTACA TGTTGAAGGG 1336  
CCTAACCAGC TTTGGGAGTA CTGACTGGTC TCTTATCTCT TAAAGCTAAG TTTTGGACTG 1396  
TGCTAATTTA CCAAATTGAT CCAGTTTGTC CTTTAGATTA AATAAGACTC GATATGAGGG 1456  
AGGGAGGGGA AGACCAGCCT CACAATGCGG CCACAGATGC CTTGCTGCTG CAGTCCTCCC 1516  
TGATCTGTCC ACTGAAGACA TGAAGTCCTC TTTTGAATGC CAAACCCACC ATTCATTGGT 1576  
GCTGACTACA TAGAATGGGG TTGAGAGAAG ATCAGTTTGG ACTTCACATT TTTGTTTTAA 1636  
GTTTTAGGTT GTTTTTTTTT GGTTTTGTTT GTTTGTTTGT TTGTTTGTTT TTGTTTTTTG 1696  
TTTTTCTTTT TTAAGTTCTT GTGGGGAAAC TTTGGGGTTA ATCAAAGGAT GTAGTCCTGT 1756  
GGTAGACCAG AGGAGTAACT AGTTTTGATC CTTTGGGGTG TGGAAAATGT ACCCAGGAAG 1816  
CTTGTGTAAG GAGGTTCTGT GACAGTGAAC ACTTCCACT TTCTGACACC TCATCCTGCT 1876  
GTACGACTCC AGGATTTGGA TTTGGATTTT TCAAATGTAG CTTGAAATTT CAATAAACTT 1936  
TGCTCCTTTT TCTAAAATA AAAAAAAAAA AAAAAA 1972

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met	Asn	Thr	Glu	Met	Tyr	Gln	Thr	Pro	Met	Glu	Val	Ala	Val	Tyr	Gln	1	5	10	15
Leu	His	Asn	Phe	Ser	Thr	Ser	Phe	Phe	Ser	Ser	Leu	Leu	Gly	Gly	Asp	20	25	30	
Val	Val	Ser	Val	Lys	Leu	Asp	Asn	Ser	Ala	Ser	Gly	Ala	Ser	Val	Val	35	40	45	
Ala	Leu	Asp	Asn	Lys	Ile	Glu	Gln	Ala	Met	Asp	Leu	Val	Lys	Asn	His	50	55	60	
Leu	Met	Tyr	Ala	Val	Arg	Glu	Glu	Val	Glu	Val	Leu	Lys	Glu	Gln	Ile	65	70	75	80
Arg	Glu	Leu	Leu	Glu	Lys	Asn	Ser	Gln	Leu	Glu	Arg	Glu	Asn	Thr	Leu	85	90	95	
Leu	Lys	Thr	Leu	Ala	Ser	Pro	Glu	Gln	Leu	Glu	Lys	Phe	Gln	Ser	Arg	100	105	110	
Leu	Ser	Pro	Glu	Glu	Pro	Ala	Pro	Glu	Ala	Pro	Glu	Thr	Pro	Glu	Thr	115	120	125	
Pro	Glu	Ala	Pro	Gly	Gly	Ser	Ala	Val	130	135									

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
 (B) LOCATION:1..20  
 (D) OTHER INFORMATION:/note= "PCR forward primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CCATCTGGGT CCACTCCAGT

20

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
 (B) LOCATION:1..20  
 (D) OTHER INFORMATION:/note= "PCR reverse primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

AGGACAGTGG GAGTGGCACC

20

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1946 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION:241..642

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

AATTCGGGGG CCGTGGAGTT TGTGACATAC GAGGTGACAC CCCTCGAGTC ACTTCCCTTC

60

AACTCCAGCT GGAGCGCCTG CTTGGCTTTG GGTTCGTTCT GCAGCCTTCG CCCCCTCCT 120

AGCCTCAGGG CCGGACTCCA GCGCAGAGCC CAGCCCAGCG CAGCCTGCCA GCAGCCACCC 180

AGCCGCCAG CCGCCAGCC CCGCACGAAA CCCGGCCAGA GCTTCCTAGC AGCCCGAGCC 240

ATG AAC ACC GAA ATG TAT CAG ACC CCC ATG GAG GTG GCG GTC TAC CAG 288  
Met Asn Thr Glu Met Tyr Gln Thr Pro Met Glu Val Ala Val Tyr Gln  
5 10 15

CTG CAC AAT TTC TCC ATC TCC TTC TTC TCT TCT CTG CTT GGA GGG GAT 336  
Leu His Asn Phe Ser Ile Ser Phe Phe Ser Ser Leu Leu Gly Gly Asp  
20 25 30

GTG GTT TCC GTT AAG CTG GAC AAC AGT GCC TCC GGA GCC AGC GTG GTG 384  
Val Val Ser Val Lys Leu Asp Asn Ser Ala Ser Gly Ala Ser Val Val  
35 40 45

GCC ATA GAC AAC AAG ATC GAA CAG GCC ATG GAT CTG GTG AAG AAT CAT 432  
Ala Ile Asp Asn Lys Ile Glu Gln Ala Met Asp Leu Val Lys Asn His  
50 55 60

CTG ATG TAT GCT GTG AGA GAG GAG GTG GAG ATC CTG AAG GAG CAG ATC 480  
Leu Met Tyr Ala Val Arg Glu Glu Val Glu Ile Leu Lys Glu Gln Ile  
65 70 75 80

CGA GAG CTG GTG GAG AAG AAC TCC CAG CTA GAG CGT GAG AAC ACC CTG 528  
Arg Glu Leu Val Glu Lys Asn Ser Gln Leu Glu Arg Glu Asn Thr Leu  
85 90 95

TTG AAG ACC CTG GCA AGC CCA GAG CAG CTG GAG AAG TTC CAG TCC TGT 576  
Leu Lys Thr Leu Ala Ser Pro Glu Gln Leu Glu Lys Phe Gln Ser Cys  
100 105 110

CTG AGC CCT GAA GAG CCA GCT CCC GAA TCC CCA CAA GTG CCC GAG GCC 624  
Leu Ser Pro Glu Glu Pro Ala Pro Glu Ser Pro Gln Val Pro Glu Ala  
115 120 125

CCT GGT GGT TCT GCG GTG TAAGTGGCTC TGTCTCAGG GTGGGCAGAG 672  
Pro Gly Gly Ser Ala Val  
130

CCACTAAACT TGTTTTACCT AGTTCTTTCC AGTTTGTTTT TGGCTCCCCA AGCATCATCT 732

CACGAGGAGA ACTTTACACC TAGCACAGCT GGTGCCAAGA GATGTCCTAA GGACATGGCC 792

ACCTGGGTCC ACTCCAGCGA CAGACCCCTG ACAAGAGCAG GTCTCTGGAG GCTGAGTTGC 852

ATGGGGCCTA GTAACACCAA GCCAGTGAGC CTCTAATGCT ACTGCGCCCT GGGGGCTCCC 912

AGGGCCTGGG CAACTTAGCT GCAACTGGCA AAGGAGAAGG GTAGTTTGAG GTGTGACACC 972

AGTTTGCTCC AGAAAGTTTA AGGGGTCTGT TTCTCATCTC CATGGACATC TTCAACAGCT 1032

TCACCTGACA ACGACTGTTT CTATGAAGAA GCCACTTGTG TTTTAAGCAG AGGCAACCTC 1092

TCTCTTCTCC TCTGTTTCGT GAAGGCAGGG GACACAGATG GGAGAGATTG AGCCAAGTCA 1152

GCCTTCTGTT GGTAAATATG GTATAATGCA TGGCTTTGTG CACAGCCCAG TGTGGGATTA 1212

CAGCTTTGGG ATGACCGCTT ACAAAGTTCT GTTTGGTTAG TATTGGCATA GTTTTTCTAT 1272

ATAGCCATAA ATGCGTATAT ATACCATAG GGCTAGATCT GTATCTTAGT GTAGCGATGT 1332

ATACATATAC ACATCCACCT ACATGTTGAA GGGCCTAACC AGCCTTGGGA GTATTGACTG 1392  
GTCCCTTACC TCTTATGGCT AAGTCTTTGA CTGTGTTTCAT TTACCAAGTT GACCCAGTTT 1452  
GTCTTTTtagg TTAAGTAAGA ACTCGAGAGT AAAGGCAAGG AGGGGGGCCA GCCTCTGAAT 1512  
GCGGCCACGG ATGCCTTGCT GCTGCAACCC TTTCCCCAGC TGTCCACTGA AACGTGAAGT 1572  
CCTGTTTTGA ATGCCAAACC CACCATTAC TGGTGCTGAC TACATAGAAT GGGTTGAGAG 1632  
AAGATCAGTT TGGGCTTCAC AGTGTCATTT GAAAAAGCGT TTTTGTTTTG TTTTGAATTA 1692  
TTGTGGAAAA CTTTCAAGTG AACAGAAGGA TGGTGTCTTA CTGTGGATGA GGGATGAACA 1752  
AGGGGATGGC TTTGATCCAA TGGAGCCTGG GAGGTGTGCC CAGAAAGCTT GTCTGTAGCG 1812  
GGTTTTGTGA GAGTGAACAC TTTCCACTTT TTGACACCTT ATCCTGATGT ATGGTTCCAG 1872  
GATTTGGATT TTGATTTTCC AAATGTAGCT TGAAATTTCA ATAACTTTG CTCTGTTTTT 1932  
CTAAAAAATA AAAA 1946

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 134 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Asn Thr Glu Met Tyr Gln Thr Pro Met Glu Val Ala Val Tyr Gln  
1 5 10 15  
Leu His Asn Phe Ser Ile Ser Phe Phe Ser Ser Leu Leu Gly Gly Asp  
20 25 30  
Val Val Ser Val Lys Leu Asp Asn Ser Ala Ser Gly Ala Ser Val Val  
35 40 45  
Ala Ile Asp Asn Lys Ile Glu Gln Ala Met Asp Leu Val Lys Asn His  
50 55 60  
Leu Met Tyr Ala Val Arg Glu Glu Val Glu Ile Leu Lys Glu Gln Ile  
65 70 75 80  
Arg Glu Leu Val Glu Lys Asn Ser Gln Leu Glu Arg Glu Asn Thr Leu  
85 90 95  
Leu Lys Thr Leu Ala Ser Pro Glu Gln Leu Glu Lys Phe Gln Ser Cys  
100 105 110  
Leu Ser Pro Glu Glu Pro Ala Pro Glu Ser Pro Gln Val Pro Glu Ala  
115 120 125  
Pro Gly Gly Ser Ala Val  
130

(2) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 amino acids

(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: pepetide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Leu Lys Glu Gln Ile Lys Glu Leu Ile Glu Lys Asn Ser Gln Leu Glu  
1 5 10 15  
Gln Glu Asn Asp Leu Leu Lys Thr Leu Ala  
20 25

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Leu Glu Asp Lys Val Glu Glu Leu Leu Ser Lys Asn Tyr His Leu Glu  
1 5 10 15  
Asn Glu Val Ala Arg Leu Lys Lys Leu Val  
20 25

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Leu Glu Asn Arg Val Ala Val Leu Glu Asn Gln Asn Lys Thr Leu Ile  
1 5 10 15  
Glu Glu Leu Lys Ala Leu Lys Asp Leu Tyr  
20 25

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Leu Glu Asn Arg Val Ala Val Leu Glu Asn Gln Asn Lys Thr Leu Ile  
1 5 10 15

Glu Glu Leu Lys Ala Leu Lys Asp Leu Tyr  
20 25

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Leu Glu Glu Lys Val Lys Thr Leu Lys Ala Gln Asn Ser Glu Leu Ala  
1 5 10 15  
Ser Thr Ala Asn Met Leu Arg Glu Gln Val  
20 25

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Met Asp Leu Val Lys Asn His Leu Met Tyr Ala Val Arg Glu Glu Val  
1 5 10 15  
Glu Ile Leu Lys Glu Gln Ile Arg Glu Leu Val Glu Lys Asn Ser Gln  
20 25 30  
Leu Glu Arg Glu Asn Thr Leu Leu Lys Thr Leu Ala Ser Pro Glu Gln  
35 40 45  
Leu Glu Lys Phe Gln Ser Cys Leu Ser Pro Glu Glu Pro Ala Pro Glu  
50 55 60  
Ser Pro Gln Val Pro Glu Ala Pro Gly Gly Ser Ala Val  
65 70 75

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

Lys Ser Gln Trp Cys Arg Pro Val Ala Met Asp Leu Gly Val Tyr Gln  
1 5 10 15  
Leu Arg His Phe Ser Ile Ser Phe Leu Ser Ser Leu Leu Gly Thr Glu  
20 25 30



Asn Ala Ser Val Arg Leu Asp Asn Ser Ser Ser Gly Ala Ser Val Val  
35 40 45

Ala Ile Asp Asn Lys Ile Glu Gln Ala Met Asp Leu Val Lys Ser His  
50 55 60

Leu Met Tyr Ala Val Arg Glu Glu Val Glu Val Leu Lys Glu Gln Ile  
65 70 75 80

Lys Glu Leu Ile Glu Lys Asn Ser Gln Leu Glu Gln Glu Asn Asn Leu  
85 90 95

Leu Lys Thr Leu Ala Ser Pro Glu Gln Leu Ala Gln Phe Gln Ala Gln  
100 105 110

Leu Gln Thr Gly Ser Pro Pro Ala Thr Thr Gln Pro Gln Gly Thr Thr  
115 120 125

Gln Pro Pro Ala Gln Pro Ala Ser Gln Gly Ser Gly Pro Thr Ala  
130 135 140

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(D) OTHER INFORMATION:/note= "the N-terminus is modified by an acetyl group; the C-terminus is modified with a-(4-methyl-coumaryl-7-amide)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Asp Glu Val Asp

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(D) OTHER INFORMATION:/note= "the N-terminus is modified by an acetyl group; the C-terminus is modified with CH<sub>2</sub>OC(O)-[2,6-(CF<sub>3</sub>)<sub>2</sub>]Ph"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

Tyr Val Ala Asp